SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: BILLING-MEDEL, PATRICIA
               COHEN, MAURICE
               COLPITTS, TRACEY L.
               FRIEDMAN, PAULA N.
               GORDON, JULIAN
               GRANADOS, EDWARD N.
               HAYDEN, MARK
               HODGES, STEVEN C.
               KLASS, MICHAEL R.
               KRATOCHVIL, JON D.
               ROBERTS-RAPP, LISA
               RUSSELL, JOHN C.
               STROUPE, STEPHEN D.

(ii) TITLE OF THE INVENTION: REAGENTS AND METHODS USEFUL
      FOR DETECTING DISEASES OF THE GASTROINTESTINAL
      TRACT

(iii) NUMBER OF SEQUENCES: 30

(iv) CORRESPONDENCE ADDRESS:
  (A) ADDRESSEE: Abbott Laboratories
  (B) STREET: 100 Abbott Park Road
  (C) CITY: Abbott Park
  (D) STATE: IL
  (E) COUNTRY: USA
  (F) ZIP: 60064-3500

(v) COMPUTER READABLE FORM:
  (A) MEDIUM TYPE: Diskette
  (B) COMPUTER: IBM Compatible
  (C) OPERATING SYSTEM: DOS
  (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
  (A) APPLICATION NUMBER: 09/052,855
  (B) FILING DATE: 31-MAR-1998
  (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
  (A) APPLICATION NUMBER: 08/828,489
  (B) FILING DATE: 31-MAR-1997

(viii) ATTORNEY/AGENT INFORMATION:
  (A) NAME: Becker, Cheryl L.
  (B) REGISTRATION NUMBER: 35,441
  (C) REFERENCE/DOCKET NUMBER: 6064.US.P1

(ix) TELECOMMUNICATION INFORMATION:
  (A) TELEPHONE: 847/935-1729
  (B) TELEFAX: 847/938-2623
  (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 273 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(ix) FEATURE:

       (A) NAME/KEY: base_polymorphism
       (B) LOCATION: 3
       (D) OTHER INFORMATION: /note= "'N' represents` an A or G or
           T or C polymorphism at this position"

  (ix) FEATURE:
       (A) NAME/KEY: base_polymorphism
       (B) LOCATION: 55
       (D) OTHER INFORMATION: /note= "'N' ·represents an A or G or
           T or C polymorphism at this position"

  (ix) FEATURE:
       (A) NAME/KEY: base_polymorphism
       (B) LOCATION: 62
       (D) OTHER INFORMATION: /note= "'N' represents an A or G or
           T or C polymorphism at this position"

  (ix) FEATURE:
       (A) NAME/KEY: base_polymorphism
       (B) LOCATION: 189
       (D) OTHER INFORMATION: /note= "'N' represents an A or G or
           T or C polymorphism at this position"

  (ix) FEATURE:
       (A) NAME/KEY: base_polymorphism
       (B) LOCATION: 201
       (D) OTHER INFORMATION: /note= "'N' represents an A or G or
           T or C polymorphism at this position"

  (ix) FEATURE:
       (A) NAME/KEY: base_polymorphism
       (B) LOCATION: 204
       (D) OTHER INFORMATION: /note= "'N' represents an A or G or
           T or C polymorphism at this position"

  (ix) FEATURE:
       (A) NAME/KEY: base_polymorphism
       (B) LOCATION: 206
       (D) OTHER INFORMATION: /note=."'N' represents an A or G or
           T or C polymorphism at this position"

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
GGNCAGAGCC TGCGCAGGGC AGGAGCAGCT GGCCCACTGG CGGCCCGCAA CACTNCGTCT      60
TNACCCTCTG GGCCCACTGC ATCTAGAGGA GGGCCGTCTG TGAGGCCACT ACCCCTCCAG     120
CAACTGGGAG GTGGGACTGT CAGAAGCTGG CCCAGGGTGG TGGTCAGCTG GGTCAGGGAC     180
CTACGGCANC TGCTGGACCA NCTNGNCTTT TCCATCGAAG CAGGGAAGTG GGAGCCTTGA     240
GCCCTTGGGT GGAAGCTTGA CCCCAAGCCA CTT                                  273
```

    (2) INFORMATION FOR SEQ ID NO:2:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 250 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (ix) FEATURE:
       (A) NAME/KEY: base_polymorphism
       (B) LOCATION: 69
       (D) OTHER INFORMATION: /note= "'N' represents an A or G or
           T or C polymorphism at this position"

  (ix) FEATURE:
       (A) NAME/KEY: base_polymorphism
       (B) LOCATION: 97

```
          (D) OTHER INFORMATION: /note= "'N' represents an A or G or
                  T or C polymorphism at this position"

  (ix)   FEATURE:
          (A) NAME/KEY: base_polymorphism
          (B) LOCATION: 140
          (D) OTHER INFORMATION: /note= "'N' represents an A or G or
                  T or C polymorphism at this position"

  (ix)   FEATURE:
          (A) NAME/KEY: base_polymorphism
          (B) LOCATION: 223
          (D) OTHER INFORMATION: /note= "'N' represents an A or G or
                  T or C polymorphism at this position"


  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGAGCCTGCG CAGGGCAGGA GCAGCTGGCC CACTGGCGGC CCGCAACACT CCGTCTCACC     60
CTCTGGGCNC ACTGCATCTA GAGGAGGGCC GTCTGTNAGG CCACTACCCC TCCAGCAACT    120
GGGAGGTGGG ACTGTCAGAN GCTGGCCCAG GGTGGTGGTC AGCTGGGTCA GGGACCTACG    180
GCACCTGCTG GACCACCTCG CCTTCTCCAT CGAAGCAGGG AANTGGGAGC CTCGAGCCCT    240
CGGGTGGAAG                                                           250

          (2) INFORMATION FOR SEQ ID NO:3:

  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 250 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

  (ix)   FEATURE:
          (A) NAME/KEY: base_polymorphism
          (B) LOCATION: 68
          (D) OTHER INFORMATION: /note= "'N' represents an A or G or
                  T or C polymorphism at this position"

  (ix)   FEATURE:
          (A) NAME/KEY: base_polymorphism
          (B) LOCATION: 232
          (D) OTHER INFORMATION: /note= "'N' represents an A or G or
                  T or C polymorphism at this position"

  (ix)   FEATURE:
          (A) NAME/KEY: base_polymorphism
          (B) LOCATION: 233
          (D) OTHER INFORMATION: /note= "'N' represents an A or G or
                  T or C polymorphism at this position"


  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGGCGGCCCG CAACACTCCG TCTCACCCTC TGGGCCCACT GCATCTAGAG GAGGGCCGTC     60
TGTGAGGNCA CTACCCCTCC AGCAACTGGG AGGTGGGACT GTCAGAATCT GGCCCAGGGT    120
GGTGGTCAGC TGGGTCAGGG ACCTACGGCA CCTGCTGGAC CACCTCGCCT TCTCCATCGA    180
AGCAGGGAAG TGGGAGCCTC GAGCCCTCGG GTGGAAGCTG ACCCCAAGCC ANNCTTCACC    240
TGGACAGGAT                                                           250

          (2) INFORMATION FOR SEQ ID NO:4:

  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 233 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
CCCTCTGGGC CCACTGCATC TAGAGGAGGG CCGTCTGTGA GGCCACTACC CCTCCAGCAA        60
CTGGGAGGTG GGACTGTCAG AAGCTGGCCC AGGGTGGTGG TCAGCTGGGT CAGGGACCTA       120
CGGCACCTGC TGGACCACCT CGCCTTCTCC ATCGAAGCAG GGAAGTGGGA GCCTCGAGCC       180
CTCGGGTGGA AGCTGACCCC AAGCCACCCT TCACCTGGAC AGGATGAGAG TGT             233
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 287 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(ix) FEATURE:
   (A) NAME/KEY: base_polymorphism
   (B) LOCATION: 17
   (D) OTHER INFORMATION: /note= "'N' represents an A or G or
          T or C polymorphism at this position"

(ix) FEATURE:
   (A) NAME/KEY: base_polymorphism
   (B) LOCATION: 60
   (D) OTHER INFORMATION: /note= "'N' represents an A or G or
          T or C polymorphism at this position"

(ix) FEATURE:
   (A) NAME/KEY: base_polymorphism
   (B) LOCATION: 193
   (D) OTHER INFORMATION: /note= "'N' represents an A or G or
          T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
CACGAGGGCC GTCTGTNAGG CCACTACCCC TCCAGCAACT GGGAGGTGGG ACTGTCAGAN        60
GCTGGCCCAG GGTGGTGGTC AGCTGGGTCA GGGACCTACG GCACCTGCTG GACCACCTCG       120
CCTTCTCCAT CGAAGCAGGG AAGTGGGAGC CTCGAGCCCT CGGGTGGAAG CTGACCCCAA       180
GCCACCCTTC ACNTGGACAG GATGAGAGTG TCAGGTGTGC TTCGCCTCCT GGCCCTCATC       240
TTTGCCATAG TCACGACATG GATGTTTATT CGAAGCTACA TGAGCTT                     287
```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 263 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
GATGTTTATT CGAAGCTACA TGAGCTTCAG CATGAAAACC ATCCGTCTGC CACGCTGGCT        60
GGCCTCGCCC ACCAAGGAGA TCCAGGTTAA AAAGTACAAG TGTGGCCTCA TCAAGCCCTG       120
CCCAGCCAAC TACTTTGCGT TTAAAATCTG CAGTGGGGCC GCCAACGTCG TGGGCCCTAC       180
TATGTGCTTT GAAGACCGCA TGATCATGAG TCCTGTGAAA AACAATGTGG GCAGAGGCCT       240
AAACATCGCC CTGGTGAATG GAA                                             263
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 228 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
GTGAAAAACA ATGTGGGCAG AGGCCTAAAC ATCGCCCTGG TGAATGGAAC CACGGGAGCT      60
GTGCTGGGAC AGAAGGCATT TGACATGTAC TCTGGAGATG TTATGCACCT AGTGAAATTC     120
CTTAAAGAAA TTCCGGGGGG TGCACTGGTG CTGGTGGCCT CCTACGACGA TCCAGGGACC     180
AAAATGAACG ATGAAAGCAG GAAACTCTTC TCTGACTTGG GGAGTTCC                  228
```

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 251 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
GGGGGGTGCA CTGGTGCTGG TGGCCTCCTA CGACGATCCA GGGACCAAAA TGAACGATGA      60
AAGCAGGAAA CTCTTCTCTG ACTTGGGGAG TTCCTACGCA AAACAACTGG GCTTCCGGGA     120
CAGCTGGGTC TTCATAGGAG CCAAAGACCT CAGGGGTAAA AGCCCCTTTG AGCAGTTCTT     180
AAAGAACAGC CCAGACACAA ACAAATACGA GGGATGGCCA GAGCTGCTGG AGATGGAGGG     240
CTGCATGCCC C                                                         251
```

(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 187 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ix) FEATURE:
      (A) NAME/KEY: base_polymorphism
      (B) LOCATION: 148
      (D) OTHER INFORMATION: /note= "'N' represents an A or G or
         T or C polymorphism at this position"

    (ix) FEATURE:
      (A) NAME/KEY: base_polymorphism
      (B) LOCATION: 185
      (D) OTHER INFORMATION: /note= "'N' represents an A or G or
         T or C polymorphism at this position"

    (ix) FEATURE:
      (A) NAME/KEY: base_polymorphism
      (B) LOCATION: 186
      (D) OTHER INFORMATION: /note= "'N' represents an A or G or
         T or C polymorphism at this position"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
GGGATGGCCA GAGCTGCTGG AGATGGAGGG CTGCATGCCC CCGAAGCCAT TTTAGGGTGG      60
CTGTGGCTCT TCCTCAGCCA GGGGCCTGAA GAAGCTCCTG CCTGACTTAG GAGTCAGAGC     120
CCGGCAGGGG CTGAGGAGGA GGAGCAGNGG GTGCTGCGTG GAAGGTGCTG CAAGTCCTTG     180
AAAGNNG                                                              187
```

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 301 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
TTTTTTTTTT TCAAAACCAG CAAAAATAAA ATTTAATTGG GCTCAAGTCT GGGCAGTTTG      60
```

```
TCCTTCCTCA GGACCAGCCG TCAGCAGTCC CTGACGAAAG CACCCCATTC TCTCCACAGA    120
CAGCTGGTTC CAGAAGGACC CTCTGAGGCT GGTCTTCCGG GTAGGATGTG CTGTGGGAGG    180
GTTCTGTTTC CGAGGAGGAG AGGCGCGACA CAGCGTGCAA GGACCTGCAG CACCTTCCAC    240
GCAGCACCCC CTGCTCCTCC TCCTCAGCCC CTGCCGGGCT CTGACTCCTA AGTCAGGCAG    300
G                                                                   301
```

        (2) INFORMATION FOR SEQ ID NO:11:

        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 123 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
TTTTTCAAAA CCAGCAAAAA TAAAATTTAA TTGGGCTCAA GTCTGGGCAG TTTGTCCTTC     60
CTCAGGACCA GCCGTCAGCA GTCCCTGACG AAAGCACCCC ATTCTCTCCA CAGACAGCTG    120
GTT                                                                 123
```

        (2) INFORMATION FOR SEQ ID NO:12:

        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 955 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

        (ix) FEATURE:
             (A) NAME/KEY: base_polymorphism
             (B) LOCATION: 946
             (D) OTHER INFORMATION: /note= "'M' represents an A or C
                  at this position"

        (ix) FEATURE:
             (A) NAME/KEY: base_polymorphism
             (B) LOCATION: 953
             (D) OTHER INFORMATION: /note= "'M' represents an A or C
                  at this position"

        (ix) FEATURE:
             (A) NAME/KEY: base_polymorphism
             (B) LOCATION: 954
             (D) OTHER INFORMATION: /note= "'M' represents an A or C
                  at this position"

        (ix) FEATURE:
             (A) NAME/KEY: base_polymorphism
             (B) LOCATION: 950
             (D) OTHER INFORMATION: /note= "'W' represents an A or T
                  at this position"

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
GATGTTTATT CGAAGCTACA TGAGCTTCAG CATGAAAACC ATCCGTCTGC CACGCTGGCT     60
GGCCTCGCCC ACCAAGGAGA TCCAGGTTAA AAAGTACAAG TGTGGCCTCA TCAAGCCCTG    120
CCCAGCCAAC TACTTTGCGT TTAAAATCTG CAGTGGGGCC GCCAACGTCG TGGGCCCTAC    180
TATGTGCTTT GAAGACCGCA TGATCATGAG TCCTGTGAAA AACAATGTGG CAGAGGCCT    240
AAACATCGCC CTGGTGAATG GAACCACGGG AGCTGTGCTG GGACAGAAGG CATTTGACAT    300
GTACTCTGGA GATGTTATGC ACCTAGTGAA ATTCCTTAAA GAAATTCCGG GGGGTGCACT    360
GGTGCTGGTG GCCTCCTACG ACGATCCAGG GACCAAAATG AACGATGAAA GCAGGAAACT    420
CTTCTCTGAC TTGGGGAGTT CCTACGCAAA ACAACTGGGC TTCCGGGACA GCTGGGTCTT    480
CATAGGAGCC AAAGACCTCA GGGGTAAAAG CCCCTTTGAG CAGTTCTTAA AGAACAGCCC    540
AGACACAAAC AAATACGAGG GATGGCCAGA GCTGCTGGAG ATGGAGGGCT GCATGCCCCC    600
GAAGCCATTT TAGGGTGGCT GTGGCTCTTC CTCAGCCAGG GGCCTGAAGA AGCTCCTGCC    660
TGACTTAGGA GTCAGAGCCC GGCAGGGGCT GAGGAGGAGG AGCAGGGGGT GCTGCGTGGA    720
```

```
AGGTGCTGCA GGTCCTTGCA CGCTGTGTCG CGCCTCTCCT CCTCGGAAAC AGAACCCTCC    780
CACAGCACAT CCTACCCGGA AGACCAGCCT CAGAGGGTCC TTCTGGAACC AGCTGTCTGT    840
GGAGAGAATG GGGTGCTTTC GTCAGGGACT GCTGACGGCT GGTCCTGAGG AAGGACAAAC    900
TGCCCAGACT TGAGCCCAAT TAAATTTTAT TTTTGCTGGT AAAAAMAAAW AAMMA         955
```

        (2) INFORMATION FOR SEQ ID NO:13:

           (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 1299 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

           (ix) FEATURE:
             (A) NAME/KEY: base_polymorphism
             (B) LOCATION: 3
             (D) OTHER INFORMATION: /note= "'N' represents an A or G or
                  T or C polymorphism at this position"

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
GGNCAGAGCC TGCGCAGGGC AGGAGCAGCT GGCCCACTGG CGGCCCGCAA CACTCCGTCT     60
CACCCTCTGG GCCCACTGCA TCTAGAGGAG GGCCGTCTGT GAGGCCACTA CCCCTCCAGC    120
AACTGGGAGG TGGGACTGTC AGAAGCTGGC CCAGGGTGGT GGTCAGCTGG GTCAGGGACC    180
TACGGCACCT GCTGGACCAC CTCGCCTTCT CCATCGAAGC AGGGAAGTGG GAGCCTCGAG    240
CCCTCGGGTG GAAGCTGACC CCAAGCCACC CTTCACCTGG ACAGGATGAG AGTGTCAGGT    300
GTGCTTCGCC TCCTGGCCCT CATCTTTGCC ATAGTCACGA CATGGATGTT TATTCGAAGC    360
TACATGAGCT TCAGCATGAA AACCATCCGT CTGCCACGCT GGCTGGCCTC GCCCACCAAG    420
GAGATCCAGG TTAAAAAGTA CAAGTGTGGC CTCATCAAGC CCTGCCCAGC CAACTACTTT    480
GCGTTTAAAA TCTGCAGTGG GGCCGCCAAC GTCGTGGGCC CTACTATGTG CTTTGAAGAC    540
CGCATGATCA TGAGTCCTGT GAAAAACAAT GTGGGCAGAG GCCTAAACAT CGCCCTGGTG    600
AATGGAACCA CGGGAGCTGT GCTGGGACAG AAGGCATTTG ACATGTACTC TGGAGATGTT    660
ATGCACCTAG TGAAATTCCT TAAAGAAATT CCGGGGGGTG CACTGGTGCT GGTGGCCTCC    720
TACGACGATC CAGGGACCAA AATGAACGAT GAAAGCAGGA AACTCTTCTC TGACTTGGGG    780
AGTTCCTACG CAAAACAACT GGGCTTCCGG GACAGCTGGG TCTTCATAGG AGCCAAAGAC    840
CTCAGGGGTA AAAGCCCCTT TGAGCAGTTC TTAAAGAACA GCCCAGCACAC AAACAAATAC    900
GAGGGATGGC CAGAGCTGCT GGAGATGGAG GGCTGCATGC CCCCGAAGCC ATTTTAGGGT    960
GGCTGTGGCT CTTCCTCAGC CAGGGGCCTG AAGAAGCTCC TGCCTGACTT AGGAGTCAGA   1020
GCCCGGCAGG GGCTGAGGAG GAGGAGCAGG GGGTGCTGCG TGGAAGGTGC TGCAGGTCCT   1080
TGCACGCTGT GTCGCGCCTC TCCTCCTCGG AAACAGAACC CTCCCACAGC ACATCCTACC   1140
CGGAAGACCA GCCTCAGAGG GTCCTTCTGG AACCAGCTGT CTGTGGAGAG AATGGGGTGC   1200
TTTCGTCAGG GACTGCTGAC GGCTGGTCCT GAGGAAGGAC AAACTGCCCA GACTTGAGCC   1260
CAATTAAATT TTATTTTTGC TGGTTTTGAA AAAAAAAA                           1299
```

        (2) INFORMATION FOR SEQ ID NO:14:

           (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 68 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
AGCTCGGAAT TCCGAGCTTG GATCCTCTAG AGCGGCCGCC GACTAGTGAG CTCGTCGACC     60
CGGGAATT                                                             68
```

        (2) INFORMATION FOR SEQ ID NO:15:

           (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 68 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AATTAATTCC CGGGTCGACG AGCTCACTAG TCGGCGGCCG CTCTAGAGGA TCCAAGCTCG   60
GAATTCCG   68

    (2) INFORMATION FOR SEQ ID NO:16:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 24 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AGCGGATAAC AATTTCACAC AGGA   24

    (2) INFORMATION FOR SEQ ID NO:17:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 18 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TGTAAAACGA CGGCCAGT   18

    (2) INFORMATION FOR SEQ ID NO:18:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 18 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGGACAGAAG GCATTTGA   18

    (2) INFORMATION FOR SEQ ID NO:19:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 19 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAACAGCCCA GACACAAAC   19

    (2) INFORMATION FOR SEQ ID NO:20:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 22 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCCAAGTCAG AGAAGAGTTT CC   22

     (2) INFORMATION FOR SEQ ID NO:21:

    (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 18 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ACTTGCAGCA CCTTCCAC   18

     (2) INFORMATION FOR SEQ ID NO:22:

    (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 23 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CAGCATGAAA ACCATCCGTC TGC   23

     (2) INFORMATION FOR SEQ ID NO:23:

    (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 24 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TTGCGTAGGA ACTCCCCAAG TCAG   24

     (2) INFORMATION FOR SEQ ID NO:24:

    (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 223 amino acids
     (B) TYPE: amino acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: None

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala Ile
1               5                   10                  15
Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser Met Lys
            20                  25                  30
Thr Ile Arg Leu Pro Arg Trp Leu Ala Ser Pro Thr Lys Glu Ile Gln
        35                  40                  45
Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro Cys Pro Ala Asn Tyr
    50                  55                  60
Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala Asn Val Val Gly Pro Thr
65                  70                  75                  80
Met Cys Phe Glu Asp Arg Met Ile Met Ser Pro Val Lys Asn Asn Val
                85                  90                  95
```

```
Gly Arg Gly Leu Asn Ile Ala Leu Val Asn Gly Thr Thr Gly Ala Val
            100                     105                 110
Leu Gly Gln Lys Ala Phe Asp Met Tyr Ser Gly Asp Val Met His Leu
        115                 120                 125
Val Lys Phe Leu Lys Glu Ile Pro Gly Gly Ala Leu Val Leu Val Ala
        130                 135                 140
Ser Tyr Asp Asp Pro Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu
145                 150                 155                     160
Phe Ser Asp Leu Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp
                165                 170                 175
Ser Trp Val Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe
                180                 185                 190
Glu Gln Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp
        195                 200                 205
Pro Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe
    210                 215                 220
```

(2) INFORMATION FOR SEQ ID NO:25:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 38 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: None

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```
Arg Trp Leu Ala Ser Pro Thr Lys Glu Ile Gln Val Lys Lys Tyr Lys
1               5                   10                  15
Cys Gly Leu Ile Lys Pro Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile
            20                  25                  30
Cys Ser Gly Ala Ala Asn
        35
```

(2) INFORMATION FOR SEQ ID NO:26:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 39 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: None

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```
Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met Ser Pro Val Lys
1               5                   10                  15
Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu Val Asn Gly Thr Thr
            20                  25                  30
Gly Ala Val Leu Gly Gln Lys
        35
```

(2) INFORMATION FOR SEQ ID NO:27:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 37 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: None

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```
Lys Glu Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp
1               5                   10                  15
Pro Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu
            20                  25                  30
Gly Ser Ser Tyr Ala
        35
```

(2) INFORMATION FOR SEQ ID NO:28:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 40 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: None

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```
Trp Val Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu
1               5                   10                  15
Gln Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro
            20                  25                  30
Glu Leu Leu Glu Met Glu Gly Cys
        35                  40
```

(2) INFORMATION FOR SEQ ID NO:29:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 8 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: None

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```
Asp Tyr Lys Asp Asp Asp Asp Lys
1               5
```

(2) INFORMATION FOR SEQ ID NO:30:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 21 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: None

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Met His Thr Glu His
1               5                   10                  15
His His His His His
        20
```